



SEQUENCE LISTING

DS  
AS  
A  
<110> STRACKE, MARY  
LIOTTA, LANCE  
SCHIFFMANN, ELLIOTT  
KRUTZCH, HENRY  
MURATA, JUN  
  
<120> AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN  
CANCER DIAGNOSIS AND THERAPY  
  
<130> 2026-4149US4  
  
<140> 09/483,831  
<141> 2000-01-17  
  
<150> 07/822,043  
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Tyr Pro Ala Phe Lys  
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*CONF*

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18

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21

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Primers

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Primers

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<210> 27  
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<223> Description of Artificial Sequence: Synthetic Peptide

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Val Leu Asn Tyr Phe  
1 5

<210> 28  
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<223> Description of Artificial Sequence: Synthetic Peptide

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Tyr Leu Asn Ala Thr

1

5

<210> 29

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<212> PRT

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<400> 29

His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr

1

5

10

<210> 30

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic Peptide

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Ser Tyr Pro Glu Ile Leu Thr Pro Ala Asp Asn

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5

10

<210> 31

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<210> 32

<211> 13

<212> PRT

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<223> Description of Artificial Sequence: Synthetic  
Peptide

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Thr Phe Pro Asn Leu Tyr Thr Phe Ala Thr Gly Leu Tyr  
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<210> 33

<211> 22

<212> PRT

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Peptide

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Val Asn Val Ile Ser Gly Pro Ile Asp Asp Tyr Asp Tyr Asp Gly Leu  
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His Asp Thr Glu Asp Lys

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<210> 34

<211> 829

<212> PRT

<213> Homo sapiens

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<223> Putative protein sequence of A2058 Autotoxin

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Cys His Asp Phe Asp Glu Leu Cys Leu Lys Thr Ala Arg Gly Trp Glu  
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Cys Thr Lys Asp Arg Cys Gly Glu Val Arg Asn Glu Glu Asn Ala Cys  
20 25 30

His Cys Ser Glu Asp Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr  
35 40 45

Gln Val Val Cys Lys Gly Glu Ser His Trp Val Asp Asp Asp Cys Glu  
50 55 60

Glu Ile Lys Ala Ala Glu Cys Pro Ala Gly Phe Val Arg Pro Pro Leu  
65 70 75 80

Ile Ile Phe Ser Val Asp Gly Phe Arg Ala Ser Tyr Met Lys Lys Gly  
85 90 95

Ser Lys Val Met Pro Asn Ile Glu Lys Leu Arg Ser Cys Gly Thr His  
100 105 110

Ser Pro Tyr Met Arg Pro Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu  
115 120 125

Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu Ser His Gly Ile Val Gly  
130 135 140

Asn Ser Met Tyr Asp Pro Val Phe Asp Ala Thr Phe His Leu Arg Gly  
145 150 155 160

Arg Glu Lys Phe Asn His Arg Trp Trp Gly Gly Gln Pro Leu Trp Ile  
165 170 175

Thr Ala Thr Lys Gln Gly Val Lys Ala Gly Thr Phe Phe Trp Ser Val  
180 185 190

Val Ile Pro His Glu Arg Arg Ile Leu Thr Ile Leu Arg Trp Leu Thr  
195 200 205

Leu Pro Asp His Glu Arg Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln  
210 215 220

Pro Asp Phe Ser Gly His Lys Tyr Gly Pro Phe Gly Pro Glu Glu Ser  
225 230 235 240

Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys Arg Pro Lys Arg Lys Val  
245 250 255

Ala Pro Lys Arg Arg Gln Glu Arg Pro Val Ala Pro Pro Lys Lys Arg  
260 265 270

Arg Arg Lys Ile His Arg Met Asp His Tyr Ala Ala Glu Thr Arg Gln  
275 280 285

Asp Lys Met Thr Asn Pro Leu Arg Glu Ile Asp Lys Ile Val Gly Gln  
290 295 300

Leu Met Asp Gly Leu Lys Gln Leu Lys Leu Arg Arg Cys Val Asn Val  
305 310 315 320

Ile Phe Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp Arg Thr  
325 330 335

Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu Val  
340 345 350

Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys  
355 360 365

Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp  
370 375 380

Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu His  
385 390 395 400

Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val Glu Arg  
405 410 415

Arg Trp His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro Ser  
420 425 430

Gly Lys Cys Phe Phe Gln Gly Asp His Gly Phe Asp Asn Lys Val Asn  
435 440 445

Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys  
450 455 460

Thr Lys Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met Cys  
465 470 475 480

Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly Ser  
485 490 495

Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met Pro Glu  
500 505 510

Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser Asp  
515 520 525

Asp Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn Lys  
530 535 540

Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr Glu Glu  
545 550 555 560

Arg His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr  
565 570 575

Asp Ile Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu Ile Phe  
580 585 590

Leu Met Leu Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln Ala Glu Val  
595 600 605

Ser Ser Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp Val Arg  
610 615 620

Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn Asp Lys  
625 630 635 640

Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro  
645 650 655

Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro Met Tyr  
660 665 670

Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys  
675 680 685

Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile  
690 695 700

Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys  
705 710 715 720

Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser  
725 730 735

Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp  
740 745 750

Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro Asp Asn  
755 760 765

Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu  
770 775 780

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr  
785 790 795 800

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
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Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile  
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<212> DNA

<213> Homo sapiens

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<223> Partial DNA sequence of A2058 Autotoxin

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2946

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<212> PRT

<213> Homo sapiens

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20 25 30

Cys Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp  
                  35                 40                 45

Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys  
 50 55 60

Gly Glu Ser His Trp Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala  
 65 70 75 80

Glu Cys Leu Gln Val Asp Ser Pro Ser Ile Asn His Leu Leu Arg Gly

85

90

95

Trp Leu Pro Met Thr Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro  
100 105 110

Asn Ile Glu Lys Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg  
115 120 125

Pro Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr  
130 135 140

Gly Leu Tyr Pro Glu Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp  
145 150 155 160

Pro Val Phe Asp Ala Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn  
165 170 175

His Arg Trp Trp Ala Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln  
180 185 190

Arg Gly Glu Ser Trp Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg  
195 200 205

Ala Glu Ile Leu Thr Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu  
210 215 220

Arg Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly  
225 230 235 240

His Lys His Met Pro Phe Gly Pro Glu Met Pro Asn Pro Leu Arg Glu  
245 250 255

Met His Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys  
260 265 270

Leu His Arg Cys Val Asn Val Ile Phe Val Glu Thr Met Asp Gly Arg  
275 280 285

Cys His Met Tyr Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val  
290 295 300

Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys  
305 310 315 320

Phe Ser Asn Asn Ala Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu  
325 330 335

Thr Cys Lys Lys Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His

340

345

350

Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile  
355 360 365

His Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp  
370 375 380

Val Tyr Lys Lys Pro Ser Gly Asn Ala Phe Ser Arg Glu Thr Thr Ala  
385 390 395 400

Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
405 410 415

Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu  
420 425 430

Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn  
435 440 445

Asn Gly Thr His Phe Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe  
450 455 460

Arg Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile  
465 470 475 480

Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys  
485 490 495

Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr  
500 505 510

Lys Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Asp Arg Pro Ala  
515 520 525

Val Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu  
530 535 540

Ser Gly Tyr Ser Glu Ile Phe Leu Met Pro Leu Trp Thr Ser Tyr Thr  
545 550 555 560

Val Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser  
565 570 575

Cys Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys  
580 585 590

Leu Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Gly Leu Gly Pro

595

600

605

Pro Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val  
610 615 620

Thr Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr  
625 630 635 640

Phe Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val  
645 650 655

Asn Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His  
660 665 670

Asp Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro  
675 680 685

Val Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr  
690 695 700

Gln Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile  
705 710 715 720

Leu Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp  
725 730 735

Glu Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg Val  
740 745 750

Arg Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser  
755 760 765

Arg Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr  
770 775 780

Glu Ser Glu Ile  
785

<210> 37  
<211> 2712  
<212> DNA  
<213> Homo sapiens

<220>  
<223> N-tera 2D1 ATX DNA sequence

<400> 37

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aatgcctgtc actgctcaga ggactgctt gccaggggag actgctgtaa caattacca 180  
gtggtttgc aaggagagtc gcattgggtt gatgatgact gtgaggaaat aaaggccgca 240  
aatgcctgc aggtttgtc gcccattt aatcatctt tccgtggatg gcttccgatg 300  
acatcataca tgaagaaagg cagcaaagtc atgcctaata ttgaaaaact aaggtcttgt 360  
ggcacacact ctccctacat gaggccggtg tacccaacta aaaccttcc taacttatac 420  
actttggcca ctgggctata tccagaatca catggaattt ttggcaattt aatgtatgt 480  
cctgtattt atgccactt tcatctgcga gggcgagaga aatttaatca tagatgggtt 540  
ggaggtcaac cgctatggat tacagccacc aagcaaagggt gtgaaagctg gaacatttt 600  
ttggctgtt gtcattccctc acgagcggag atattaacca tattgcgtt gtcaccctt 660  
ccagatcatg agaggccctt ggtctatgcc ttcttattctt agcaaccttga ttctcttgg 720  
cacaacata tgccttcgg ccctgagatg acaaattctc tgaggaaat gcacaaaattt 780  
gtggggcaat taatggatgg actgaaacaa ctaaaactgc atcggtgtt caacgtcatc 840  
tttgcgaga ccatggatgg aagatgtcac atgtatagaa ctgagttctt gagtaatttt 900  
ctaactaatg tggatgatat tactttatgt ccttggactc taggaagaat tcgatccaa 960  
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gcttggatgtt ttagtggaaatg cttctaaatg gtgctgcaga tttgatattt gatttggaa 2640  
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2712

<210> 38  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 38  
Arg Val Trp Asn Tyr Phe Gln Arg  
1 5

<210> 39  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 39  
Met His Thr Ala Arg Val Arg Asp  
1 5

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 40  
Phe Ser Asn Asn Ala Lys Tyr Asp  
1 5

<210> 41  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 41

Val Met Pro Asn Ile Glu Lys

1

5

<210> 42

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 42

Thr Ala Arg Gly Trp Glu Cys Thr

1

5

<210> 43

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<220>

<221> VARIANT

<222> (1)

<223> Xaa represents either an unknown or any amino acid residue.

<220>

<221> VARIANT

<222> (7)

<400> 43

Xaa Asp Ser Pro Trp Thr Xaa Ile Ser Gly Ser

1

5

10

<210> 44  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 44  
Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met  
1 5 10

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 45  
Thr Tyr Leu His Thr Tyr Glu Ser  
1 5

<210> 46  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 46  
Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln  
1 5 10

<210> 47  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 47  
Ile Val Gly Gln Leu Met Asp Gly  
1 5

<210> 48  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 48  
Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
1 5

<210> 49  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 49  
Gln Ala Glu Val Ser Ser Val Pro Asp  
1 5

<210> 50  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 50  
Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys  
1 5 10

<210> 51  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 51  
Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu  
1 5 10

<210> 52  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 52  
Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro  
1 5 10 15

<210> 53  
<211> 117  
<212> DNA  
<213> Homo sapiens

<220>  
<223> 5' end of human liver ATX gene

<400> 53  
atggcaagga ggagctcggtt ccagtcgtgt caagatataat ccctgttcac ttttgccgtt 60  
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgg 117

<210> 54  
<211> 39  
<212> PRT  
<213> Homo sapiens

<220>

<223> N-terminal region including transmembrane domain  
of liver ATX protein

<400> 54

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg Ala Glu Gly Trp  
35

<210> 55

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 55

gctcagataa ggagggaaaga g 21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 56

gaatccgtag gacatctgct t 21

<210> 57

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 57  
ttagggccaa acagttctga c

21

<210> 58  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> variation  
<222> (3)  
<223> Base y represents t/u or c.

<220>  
<221> variation  
<222> (6)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (12)  
<223> Base r represents g or a.

<220>  
<221> variation  
<222> (15)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (18)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (21)  
<223> Base y represents c or t/u.

<220>  
<221> variation  
<222> (24)

*OS*  
*cont.*

<223> Base n represents inosine.

<400> 58  
aaytcnatgc aracngtntt ygtng

25

<210> 59  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> variation  
<222> (3)  
<223> Base y represents c or t/u.

<220>  
<221> variation  
<222> (6)  
<223> Base n represents inosine..

<220>  
<221> variation  
<222> (9)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (12)  
<223> Base y represents c or t/u.

<220>  
<221> variation  
<222> (15)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (18)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (21)

<223> Base n represents inosine.

<220>

<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 59

ttygtngnt ayggncnac nttyaa

26

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Basen y represents c or t/u.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)

<223> Base n represents inosine.

<220>

<221> variation

<222> (12)

<223> Base n represents inosine.

<220>

<221> variation

<222> (15)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (18)

<223> Base n represents inosine.

<220>

<221> variation

<222> (21)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 60

aaytayctna cnaaygtnga ygayat

26

PS  
cont.

<210> 61

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)

<223> Base n represents inosine.

<220>

<221> variation

<222> (12)

<223> Base n represents inosine.

<220>

<221> variation

<222> (15)

<223> Base n represents inosine.

<220>

<221> variation

<222> (18)

<223> Base n represents inosine..

<220>

<221> variation

<222> (21)

<223> Base n represents inosine.

<220>

<221> variation

<222> (24)

<223> Base n represents inosine.

<400> 61

gaygayatna cnctngtncc nggnac

26

<210> 62

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents t/u or c.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)..(10)

<223> Base r represents a or g. Base y represents c  
or t/u.

<220>

<221> variation

<222> (12)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (15)  
<223> Base r represents a or g.

<220>  
<221> variation  
<222> (18)  
<223> Base r represents a or g.

<220>  
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<222> (21)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (24)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (27)  
<223> Base n represents inosine.

<400> 62  
tgyttagtgc tncargargc nggnccncc

29

<210> 63  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Putative autotoxin protein sequence from human  
liver

<220>  
<221> VARIANT  
<222> (860)  
<223> Xaa at positions: 860, 889, 905, 911, 927, 937,  
944, 950, 954, 967, 975 represents either an  
unknown or any amino acid residue.

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 63  
gctgtcttca aacacagc 18

<210> 64  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 64  
ctgggtggctg taatccatag c 21

<210> 65  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 65  
cgtgaaggca aagagaacac g 21

<210> 66  
<211> 3104  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Polynucleotide

<400> 66  
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gagtcaatat ctgcttagga ttcactgcac atcgaattaa gagagcagaa gatgggagg 180  
aaggcctcc tacagtgcta tcagactccc cctggaccaa catctccgga tcttgcaagg 240

gcaggtgctt tgaactcaa gaggctggac ctccgttgc aacttgtgt 300  
agagctatac cagttgtgc catgactttg atgagctgtg tttgaagaca gcccgtgcgt 360  
gggagtgtac taaggacaga tgtggagaag tcagaaatga agaaaatgcc tgcactgtc 420  
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aaggcagcaa agtcatgcct aatattgaaa aactaaggc ttgtggcaca cactcgcccc 660  
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tatatccaga atcacatgga attgttgca attcaatgtt tgatccgtt tttgatgcca 780  
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ttttgttattt attaatttga aaccaggaca taaaatgt tagtattta atccctgtacc 2760  
aaatctgaca tattatgcct gaatgactcc actgttttcc tctaattgtt gatggatgtt 2820  
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tctaaatggt gctgcagatt tgatattgc attgaggaaa tattaatttt ccaatgcaca 2940  
gttgccacat ttatgttgc actgtatgga aacactgatt ttgtaaagtt gcctttattt 3000  
gctgttaact gttaactatg acagatataat ttaaggccta taaaccaatc taaacataaa 3060  
taaatcacac attcagttt ttctggtaaaa aaaaaaaaaaaa aaaa

3104

<210> 67  
<211> 861  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Polypeptide

<400> 67  
Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser  
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe  
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys  
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys  
85 90 95

Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg  
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly  
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp  
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Pro Ala Gly  
145 150 155 160

Phe Val Arg Pro Pro Leu Ile Ile Phe Ser Val Asp Gly Phe Arg Ala  
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu  
180 185 190

Arg Ser Cys Gly Thr His Ser Pro His Met Arg Pro Val Tyr Pro Thr  
195 200 205

Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu  
210 215 220

Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala  
225 230 235 240

Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly  
245 250 255

Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Arg Gly Glu Ser Trp  
260 265 270

Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg Ala Glu Ile Leu Thr  
275 280 285

Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu Arg Leu Arg Ser Met  
290 295 300

Pro Ser Ile Leu Ser Asn Leu Ile Ser Leu Asp Thr Asn Met Pro Phe  
305 310 315 320

Gly Pro Glu Met Thr Asn Pro Leu Arg Glu Ile Asp Lys Ile Val Gly  
325 330 335

Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu His Arg Cys Val Asn  
340 345 350

Val Ile Phe Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp Arg  
355 360 365

Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu  
370 375 380

Val Pro Gly Thr Leu Gly Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys  
385 390 395 400

Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp  
405 410 415

Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu His  
420 425 430

Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val Glu Arg  
435 440 445

Arg Trp His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro Ser  
450 455 460

Gly Lys Cys Phe Phe Gln Gly Asp His Gly Phe Asp Asn Lys Val Asn  
465 470 475 480

Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys  
485 490 495

Thr Lys Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met Cys  
500 505 510

Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly Ser  
515 520 525

Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met Pro Glu  
530 535 540

Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser Asp  
545 550 555 560

Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn Lys  
565 570 575

Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr Glu Glu  
580 585 590

Arg His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr  
595 600 605

Asp Val Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu Ile Phe  
610 615 620

Leu Met Pro Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln Ala Glu Val  
625 630 635 640

Ser Ser Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp Val Arg  
645 650 655

Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn Asp Lys  
660 665 670

Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro  
675 680 685

Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro Met Tyr  
690 695 700

Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys  
705 710 715 720

Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile  
725 730 735

Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys  
740 745 750

Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser  
755 760 765

Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp  
770 775 780

Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Arg His Arg Pro Asp Asn  
785 790 795 800

Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu  
805 810 815

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr  
820 825 830

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
835 840 845

Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile  
850 855 860

<210> 68

<211> 3251

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polynucleotide

<400> 68

cgtgaaggca aagagaacac gctgcaaaag gcttccaaga atcctcgaca tggcaaggag 60  
gagctcgttc cagtcgtgtc agataatatc cctgttcaact tttgccgttg gagtcagtat 120  
ctgcttagga ttcactgcac atcgaattaa gagagcagaa ggatgggagg aaggccctcc 180  
tacagtgcta tcagactccc cctggaccaa catctccgga tcttgcagg gcagggtgctt 240  
tgaacttcaa gaggctggac ctcctgattg tcgctgtgac aacttgtgta agagctatac 300  
cagttgctgc catgactttg atgagctgtg tttgaagaca gcccgtggct gggagtgtac 360  
taaggacaga tgtggagaag tcagaaatgca agaaaaatgcc tgtcactgct cagaggactg 420

cttggccagg ggagactgct gtaccaatta ccaagtggtt tgcaaaggag agtcgcattg 480  
ggttcatat gactgtgagg aaataaaggc cgcagaatgc cctgcagggt ttgttcgccc 540  
tccattaatc atcttctccg tggatggctt ccgtgcatca tacatgaaga aaggcagcaa 600  
agtcatgcct aatattgaaa aactaaggc ttgtggcaca cactctccct acatgaggcc 660  
ggtgtaccca actaaaacctt ttcctaactt atacactttg gccactggc tatatccaga 720  
atcacatgga attgttggca attcaatgta tgatcctgta tttgatgcca cttttcatct 780  
gcgagggcga gagaaattta atcatagatg gtggggaggt caaccgctat ggattacagc 840  
caccaagcaa ggggtgaaag ctgaaacattt ctttggctt gttgtcatcc ctcacgagcg 900  
gagaatatta accatattgc ggtggctcac cctgccagat catgagaggc cttcggtcta 960  
tgcccttat tctgagcaac ctgatttctc tggacacaaa tatggccctt tcggccctga 1020  
ggagagtagt tatggctcac ctttactcc ggctaagaga cctaagagga aagttgcccc 1080  
taagaggaga cagggaaagac cagttgctcc tccaaagaaaa agaagaagaa aaatacatag 1140  
gatggatcat tatgctgcgg aaactcgta ggacaaaatg acaaattcctc tgagggaaat 1200  
cgacaaaatt gtggggcaat taatggatgg actgaaacaa ctaaaactgc gtcgggtgt 1260  
caacgtcattt tttgtcgag accatggaaat ggaagatgto acatgtgata gaactgagtt 1320  
ctttagtaat tacctaacta atgtggatga tattactta gtgcctggaa ctctaggaag 1380  
aattcgatcc aaatttagca acaatgctaa atatgacccc aaagccattt tgccaaatct 1440  
cacgtgtaaa aaaccagatc agcactttaa gccttacttg aaacagcacc ttcccaaacg 1500  
tttgcactat gccaacaaca gaagaattga ggatatccat ttattggtgg aacgcagatg 1560  
gcatgttgcg aggaaacctt tggatgttta taagaaacca tcaggaaaat gcttttcca 1620  
gggagaccac ggatttgata acaaggtcaa cagcatgcag actgttttg taggttatgg 1680  
cccaacattt aagtacaaga ctaaagtgc tccatttggaa aacattgaac ttacaatgt 1740  
tatgtgtgat ctccctggat tgaagccagc tcctaataat gggacccatg gaagtttggaa 1800  
tcatctcctg cgcactaata ccttcagcc aaccatgcca gaggaagtta ccagacccaa 1860  
ttatccaggg attatgtacc ttcagtcgat tttgacactg ggctgcactt gtgtatgataa 1920  
ggtagagcca aagaacaagt tggatgaact caacaaacgg cttcatacaa aagggtctac 1980  
agaagagaga cacccctct atgggcgacc tgcagtgcctt tattcgacta gatatgat 2040  
cttatatcac actgactttg aaagtggta tagtggaaata ttcctaattgc tactctggac 2100  
atcatataact gttccaaac aggctgaggt ttccagcgtt cctgaccatc tgaccagttg 2160  
cgtccggcct gatgtccgtg tttctccgag tttcagtcgaaactgtttgg cctacaaaaa 2220  
tgataagcag atgtcctacg gattccttcc tcccttctt ctgagcttcc caccagaggg 2280  
taaatatgat gcattccttgc taaccaatat ggttccaaatg tattcctgcctt tcaaacgggt 2340  
ctggaattat ttccaaaggg tattggtaa gaaatatgct tcggaaagaa atggagttaa 2400  
cgtgataagt ggaccaatct tcgactatgaa ctatgatggc ttacatgaca cagaagacaa 2460  
aataaaaacag tacgtggaaag gcagttccat tcctgttcca actcactact acagcatcat 2520  
caccagctgt ctggatttca ctcagcctgc cgacaagtgt gacggccctc tctctgtgtc 2580  
ctcccttcattc ctgccttcacc ggcctgacaa cgaggagagc tgcaatagct cagaggacga 2640  
atcaaaaatgg gtggaaagac tcatgaaatgc gcacacagct agggtgcgtg acattgaaca 2700  
tctcaccaggc ctggacttct tccgaaagac cagccgcagc tacccagaaa tcttgacact 2760  
caagacatac ctgcatacat atgagagcga gatttaactt tctgagcattc tgcaatgac 2820  
tcttatcaac tggatgtata tttttatatt gttttgtat ttattaattt gaaaccagga 2880  
cattaaaaat gttatgtattt taatcctgta ccaaatctga catattatgc ctgaatgact 2940  
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aaatactgca gcttgagaaaa aagtggaaagc ttctaaatgg tgctgcagat ttgatattt 3060  
cattgaggaa atattaattt tccaatgcac agtggccaca tttatgttgc tactgtatgg 3120  
aaacactgat tttgtaaatgt tgcctttatt tgctgttaac tgttaactat gacagatata 3180  
tttaaggcattt ataaaccaat cttaaacaata ataaatcaca cattcagttt taaaaaaaaa 3240  
aaaaaaaaaa a

3251

<210> 69  
<211> 915  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polypeptide

<400> 69

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Ser Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg' Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser  
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe  
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys  
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys  
85 90 95

Thr Ala Arg Gly Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg  
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly  
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp  
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Pro Ala Gly  
145 150 155 160

Phe Val Arg Pro Pro Leu Ile Ile Phe Ser Val Asp Gly Phe Arg Ala  
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu  
180 185 190

Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro Val Tyr Pro Thr  
195 200 205

Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu  
210 215 220

Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala  
225 230 235 240

Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly  
245 250 255

Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Gly Val Lys Ala Gly  
260 265 270

Thr Phe Phe Trp Ser Val Val Ile Pro His Glu Arg Arg Ile Leu Thr  
275 280 285

Ile Leu Arg Trp Leu Thr Leu Pro Asp His Glu Arg Pro Ser Val Tyr  
290 295 300

Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly His Lys Tyr Gly Pro  
305 310 315 320

Phe Gly Pro Glu Glu Ser Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys  
325 330 335

Arg Pro Lys Arg Lys Val Ala Pro Lys Arg Arg Gln Glu Arg Pro Val  
340 345 350

Ala Pro Pro Lys Lys Arg Arg Lys Ile His Arg Met Asp His Tyr  
355 360 365

Ala Ala Glu Thr Arg Gln Asp Lys Met Thr Asn Pro Leu Arg Glu Ile  
370 375 380

Asp Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu  
385 390 395 400

Arg Arg Cys Val Asn Val Ile Phe Val Gly Asp His Gly Met Glu Asp  
405 410 415

Val Thr Cys Asp Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val  
420 425 430

Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys  
435 440 445

Phe Ser Asn Asn Ala Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu  
450 455 460

Thr Cys Lys Lys Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His  
465 470 475 480

Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile  
485 490 495

His Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp  
500 505 510

Val Tyr Lys Lys Pro Ser Gly Lys Cys Phe Phe Gln Gly Asp His Gly  
515 520 525

Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
530 535 540

Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu  
545 550 555 560

Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn  
565 570 575

Asn Gly Thr His Gly Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe  
580 585 590

Arg Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile  
595 600 605

Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys  
610 615 620

Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr  
625 630 635 640

Lys Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Arg Pro Ala Val  
645 650 655

Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu Ser  
660 665 670

Gly Tyr Ser Glu Ile Phe Leu Met Leu Leu Trp Thr Ser Tyr Thr Val  
675 680 685

Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser Cys  
690 695 700

Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu  
705 710 715 720

Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro  
725 730 735

Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr  
740 745 750

Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe  
755 760 765

Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn  
770 775 780

Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp  
785 790 795 800

Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val  
805 810 815

Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln  
820 825 830

Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu  
835 840 845

Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu  
850 855 860

Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg  
865 870 875 880

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg  
885 890 895

Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu  
900 905 910

Ser Glu Ile  
915

<210> 70  
<211> 979  
<212> PRT  
<213> Homo sapiens

<220>

<223> Putative autotoxin protein sequence from human liver.

<220>

<221> VARIANT

<222> (860)

<223> Xaa at positions: 860, 889, 905, 911, 927, 937, 944, 950, 954, 967, and 975 represents an unknown or other amino acid.

*John*  
<400> 70

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser  
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe  
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys  
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys  
85 90 95

Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg  
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly  
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp  
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Leu Gln Val  
145 150 155 160

Cys Ser Pro Ser Ile Asn His Leu Leu Arg Gly Trp Leu Pro Met Thr  
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu  
180 185 190

Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro Val Tyr Pro Thr  
195 200 205

Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu  
210 215 220

Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala  
225 230 235 240

Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly  
245 250 255

Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Arg Gly Glu Ser Trp  
260 265 270

Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg Ala Glu Ile Leu Thr  
275 280 285

Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu Arg Pro Ser Val Tyr  
290 295 300

Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly His Lys His Met Pro  
305 310 315 320

Phe Gly Pro Glu Met Thr Asn Pro Leu Arg Glu Met His Lys Ile Val  
325 330 335

Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu His Arg Cys Val  
340 345 350

Asn Val Ile Phe Val Glu Thr Met Asp Gly Arg Cys His Met Tyr Arg  
355 360 365

Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu  
370 375 380

Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys Phe Ser Asn Asn Ala  
385 390 395 400

Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro  
405 410 415

Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu  
420 425 430

His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val Glu  
435 440 445

Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro  
450 455 460

Ser Gly Asn Ala Phe Ser Arg Glu Thr Thr Ala Phe Asp Asn Lys Val  
465 470 475 480

Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys Tyr  
485 490 495

Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met  
500 505 510

Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly  
515 520 525

Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met Pro  
530 535 540

Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser  
545 550 555 560

Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn  
565 570 575

Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr Glu  
580 585 590

Glu Arg His Leu Leu Tyr Gly Asp Arg Pro Ala Val Leu Tyr Arg Thr  
595 600 605

Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu  
610 615 620

Ile Phe Leu Met Pro Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln Ala  
625 630 635 640

Glu Val Ser Ser Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp  
645 650 655

Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn  
660 665 670

Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser  
675 680 685

Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro  
690 695 700

Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu  
705 710 715 720

Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly  
725 730 735

Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys  
740 745 750

Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr  
755 760 765

Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys  
770 775 780

Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro  
785 790 795 800

Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val  
805 810 815

Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His  
820 825 830

Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu  
835 840 845

Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile Xaa  
850 855 860

Leu Ser Glu His Leu Gln Tyr Ser Leu Ile Asn Trp Leu Tyr Ile Phe  
865 870 875 880

Ile Leu Phe Leu Tyr Leu Leu Ile Xaa Asn Gln Asp Ile Lys Asn Val  
885 890 895

Ser Ile Leu Ile Leu Tyr Gln Ile Xaa His Ile Met Pro Glu Xaa Leu  
900 905 910

His Cys Phe Ser Leu Met Leu Asp Leu Gly Ser Leu Val Phe Xaa Val  
915 920 925

Glu Leu Val Ile Asn Thr Ala Ala Xaa Val Phe Ser Gly Ser Phe Xaa  
930 935 940

Met Val Leu Gln Ile Xaa Tyr Leu His Xaa Gly Asn Ile Asn Phe Pro  
945 950 955 960

Met His Ser Cys His Ile Xaa Ser Cys Thr Val Trp Lys His Xaa Phe  
965 970 975

Cys Lys Val

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PS